

# Appendix III

Alignment of SEQ ID NO: 1479 of Tang et al with the sequence of GenBank Accession No. BAA23691.2

>gb|BAA23691.2| KIAA0395 [Homo sapiens]  
Length=879

Score = 1827 bits (4732), Expect = 0.0, Method: Compositional matrix adjust.  
Identities = 877/879 (99%), Positives = 878/879 (99%), Gaps = 0/879 (0%)

Query	78	SCKYCDPRSHDMTOFVGHMNSHHTDFNKDPTFVCSGCSFLAKTEPEGLSLHMATCHSGEAS	137
Sbjct	1	SCKYCDPRSHDMTOFVGHMNSHHTDFNKDPTFVCSGCSFLAKTEPEGLSLHMATCHSGEAS	60
Query	138	FVMNVAKPDNHVVVEQSIPBSTSTPDLAGEPSARGADGOAEIIITKTPIMKIMKGKAEAK	197
Sbjct	61	FVMNVAKPDNHVVVEQSIPBSTSTPDLAGEPSARGADGOAEIIITKTPIMKIMKGKAEAK	120
Query	198	KIHTLKENVPSPQVGEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGPL	257
Sbjct	121	KIHTLKENVPSPQVGEALFKLSTGEMEVREGDHSFINGAVFVSQASASSAKNPHAANGPL	180
Query	258	IGTVFLPAGIAQFLSLQQQFPVHAQHVVHQFLPTAKALPKVMIPLSSIPTTAAAMDSNS	317
Sbjct	181	IGTVFLPAGIAQFLSLQQQFPVHAQHVVHQFLPTAKALPKVMIPLSSIPTTAAAMDSNS	240
Query	318	FLKNSFHKKFPYPTKAECLYTVVTKYPEEQLKIWPTAQRLKQGISMSPEIEHARKMFTN	377
Sbjct	241	FLKNSFHKKFPYPTKAECLYTVVTKYPEEQLKIWPTAQRLKQGISMSPEIEHARKMFTN	300
Query	378	TVIQSVPOPTITVLNTPLVASAGNVQHLQAALPGHVVGQPEGTGGGLLVTPQLMANGQL	437
Sbjct	301	TVIQSVPOPTITVLNTPLVASAGNVQHLQAALPGHVVGQPEGTGGGLLVTPQLMANGQL	360
Query	438	ATSSLEPLIVTSVPKQGVAPINTVCSNTTSVAVKVVNAQOSLLTACPSITSOAFLDASII	497
Sbjct	361	ATSSLEPLIVTSVPKQGVAPINTVCSNTTSVAVKVVNAQOSLLTACPSITSOAFLDASII	420
Query	498	KNKKSHQQLSALKGSPCRNQFFGQSEVEHLTKVTGLSTREVRKMPSDRRYHCRNLKGSRA	557
Sbjct	421	KNKKSHQQLSALKGSPCRNQFFGQSEVEHLTKVTGLSTREVRKMPSDRRYHCRNLKGSRA	480
Query	558	MIPGDHSSIIDSVPVSVSPSSKVPVETCIPPTATLATHPSAKRQSMHQTPDPTTKYK	617
Sbjct	481	MIPGDHSSIIDSVPVSVSPSSKVPVETCIPPTATLATHPSAKRQSMHQTPDPTTKYK	540
Query	618	ERAPQLRALSSSTAQNPLDRLDRLSETKMTREIDSMFSERRKKVNAEETTKAEZ	677
Sbjct	541	ERAPQLRALSSSTAQNPLDRLDRLSETKMTREIDSMFSERRKKVNAEETTKAEZ	600
Query	678	NASQEEEEAADEGGEDLASLRLVSGENGSELEMPSSHILAEKRVSPKIKILNKLRLVTEA	737
Sbjct	601	NASQEEEEAADEGGEDLASLRLVSGENGSELEMPSSHILAEKRVSPKIKILNKLRLVTEA	660
Query	738	NGRNEIPGLGACDPEDDESNIARQLPGKVSCKKTAQQRHLLRLQFLVQPMNSHQDYSLI	797
Sbjct	661	NGRNEIPGLGACDPEDDESNIARQLPGKVSCKKTAQQRHLLRLQFLVQPMNSHQDYSLI	720
Query	798	MAQTGLPRPEVVMFGDSRYALNGQLKWYEDYKRWFPFGLLVIAFGHRLQLQDYTMTH	857
Sbjct	721	MAQTGLPRPEVVMFGDSRYALNGQLKWYEDYKRWFPFGLLVIAFGHRLQLQDYTMTH	780
Query	858	KMLYEEDLQMLCDKTQSSQGVKQWFAEKMGEETRAVADTGSFQGGFGLDVAHKGWG	917
Sbjct	781	KMLYEEDLQMLCDKTQSSQGVKQWFAEKMGEETRAVADTGSFQGGFGLDVAHKGWG	840
Query	918	DTYSEVSENSSESWEPVPEASSEFPDTSSPQAGRQLETD	956
Sbjct	841	DTYSEVSENSSESWEPVPEASSEFPDTSSPQAGRQLETD	879